

**AMENDMENTS TO THE CLAIMS**

1. (Withdrawn) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Loop Consensus Sequence 15: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Cys (TN8), wherein

X<sub>2</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;  
X<sub>3</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>4</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);  
X<sub>5</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>6</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and  
X<sub>7</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys (TN12), wherein

X<sub>2</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;  
X<sub>3</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;  
X<sub>4</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>5</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;  
X<sub>6</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>7</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;  
X<sub>9</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>10</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and  
X<sub>11</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Gly-X<sub>6</sub>-Cys (TN7), wherein

X<sub>2</sub> is Asn, Asp or Glu;  
X<sub>3</sub> is Glu, His, Lys or Phe;  
X<sub>4</sub> is Asp, Gln, Leu, Lys, Met or Tyr; and

X<sub>6</sub> is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (TN9), wherein

X<sub>2</sub> is Ala, Asp, Lys, Ser, Trp or Val;

X<sub>3</sub> is Asn, Glu, Gly, His or Leu;

X<sub>4</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X<sub>5</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X<sub>6</sub> is His, Pro or Trp;

X<sub>7</sub> is Ala, Gly, His, Leu, Trp or Tyr; and

X<sub>8</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Ser-Gly-Pro-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys

(MTN13; SEQ ID NO:1), wherein

X<sub>2</sub> is Asp, Glu, His or Thr;

X<sub>3</sub> is Arg, His, Lys or Phe;

X<sub>4</sub> is Gln, Ile, Lys, Tyr or Val;

X<sub>5</sub> is Gln, Ile, Leu, Met or Phe;

X<sub>9</sub> is Asn, Asp, Gly, His or Tyr;

X<sub>10</sub> is Gln, Gly, Ser or Thr;

X<sub>11</sub> is Glu, Lys, Phe or Ser; and

X<sub>12</sub> is Glu, Ile, Ser or Val.

2. (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 20: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-Tyr-Cys (TN8), wherein

X<sub>2</sub> is Ala, Arg, Glu, Lys or Ser;

X<sub>3</sub> is Ala, Asp, Gln, Glu, Thr or Val;

X<sub>4</sub> is Asp or Glu;

X<sub>5</sub> is Trp or Tyr; and

X<sub>6</sub> is Thr or Tyr; or

Loop Consensus Sequence 21: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Gly-X<sub>6</sub>-X<sub>7</sub>-Cys (TN8), wherein

X<sub>2</sub> is Asp, Gln or His;  
X<sub>3</sub> is His or Tyr;  
X<sub>4</sub> is His, Ile or Tyr;  
X<sub>6</sub> is Ile, Met or Val; and  
X<sub>7</sub> is Gly or Tyr; or

Loop Consensus Sequence 22: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Gly-X<sub>7</sub>-Cys (TN8), wherein

X<sub>2</sub> is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;  
X<sub>3</sub> is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;  
X<sub>4</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr or Val;  
X<sub>5</sub> is Asp, Phe, Ser, Thr, Trp or Tyr; and  
X<sub>7</sub> is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr.

3. (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of one of the following:

Loop Consensus Sequence 23: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Trp-Gly-Gly-X<sub>9</sub>-X<sub>10</sub>-Cys (SEQ ID NO:3; TN11), wherein

X<sub>2</sub> is Ala, Phe or Trp;  
X<sub>3</sub> is Glu or Lys;  
X<sub>4</sub> is Asp, Ser, Trp or Tyr;  
X<sub>5</sub> is Phe, Pro or Ser;  
X<sub>9</sub> is Gln or Glu; and  
X<sub>10</sub> is Ile, Phe or Val; or

Loop Consensus Sequence 24: Cys-X<sub>2</sub>-Glu-X<sub>4</sub>-Ser-X<sub>6</sub>-Ser-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Phe-Cys (SEQ ID NO:15; TN12), wherein

X<sub>2</sub> is His or Tyr;  
X<sub>4</sub> is Leu, His or Thr;  
X<sub>6</sub> is Asp or Leu;  
X<sub>8</sub> is Gly or Val;  
X<sub>9</sub> is Thr or Val; and

X<sub>10</sub> is Arg or Trp; or

Loop Consensus Sequence 25: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Gly-X<sub>9</sub>-Trp-X<sub>11</sub>-Cys (TN12; SEQ ID NO:16), wherein

X<sub>2</sub> is Glu, Met or Thr;

X<sub>3</sub> is Ile, Leu, Met or Phe;

X<sub>4</sub> is Arg, Asp, Glu, Met, Trp or Val;

X<sub>5</sub> is Asn, Gln, Gly, Ser or Val;

X<sub>6</sub> is Glu or Asp;

X<sub>7</sub> is Lys, Ser, Thr or Val;

X<sub>9</sub> is Arg, Gln, Lys or Trp; and

X<sub>11</sub> is Asn, Leu, Phe or Tyr; or

Loop Consensus Sequence 26: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys (TN12), wherein

X<sub>2</sub> is Glu or Gly;

X<sub>3</sub> is Trp or Tyr;

X<sub>4</sub> is Ser or Thr;

X<sub>5</sub> is Asn or Gln;

X<sub>6</sub> is Gly or Met;

X<sub>7</sub> is Phe or Tyr;

X<sub>8</sub> is Asp or Gln;

X<sub>9</sub> is Lys or Tyr;

X<sub>10</sub> is Glu or Thr; and

X<sub>11</sub> is Glu or Phe.

4. (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 27: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Gly-X<sub>6</sub>-Cys (TN7), wherein

X<sub>2</sub> is Asn, Asp or Glu;

X<sub>3</sub> is Glu, His, Lys or Phe;

X<sub>4</sub> is Asp, Gln, Leu, Lys, Met or Tyr; and  
X<sub>6</sub> is Arg, Gln, Leu, Lys or Val.

5. (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 28: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (TN9), wherein

X<sub>2</sub> is Ala, Lys, Ser, Trp or Val;  
X<sub>3</sub> is Asn, Glu, Gly, His or Leu;  
X<sub>4</sub> is Glu, Gly, Lys, Met or Tyr;  
X<sub>5</sub> is Ala, Asn, Asp, Leu, Met, Pro or Ser;  
X<sub>6</sub> is His, Pro or Trp;  
X<sub>7</sub> is His, Leu, Trp or Tyr; and  
X<sub>8</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp.

6. (Withdrawn) The polypeptide of Claim 1, wherein the polypeptide comprises an amino acid sequence of the following:

Loop Consensus Sequence 29: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Ser-Gly-Pro-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys (SEQ ID NO:1; MTN13), wherein

X<sub>2</sub> is Asp, Glu, His or Thr;  
X<sub>3</sub> is Arg, His, Lys or Phe;  
X<sub>4</sub> is Gln, Ile, Lys, Tyr or Val;  
X<sub>5</sub> is Gln, Ile, Leu, Met or Phe;  
X<sub>9</sub> is Asn, Asp, Gly, His or Tyr;  
X<sub>10</sub> is Gln, Gly, Ser or Thr;  
X<sub>11</sub> is Glu, Lys, Phe or Ser; and  
X<sub>12</sub> is Glu, Ile, Ser or Val.

7. (Withdrawn) An isolated polypeptide having the ability to bind to KDR or VEGF/KDR complex comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (TN8),  
wherein

X<sub>1</sub> is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>2</sub> is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>3</sub> is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;  
X<sub>5</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;  
X<sub>6</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp,  
Tyr or Val;  
X<sub>7</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>9</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;  
X<sub>10</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;  
X<sub>12</sub> is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr  
or Val;  
X<sub>13</sub> is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or  
Tyr; and  
X<sub>14</sub> is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-  
X<sub>18</sub> (TN12), wherein

X<sub>1</sub> is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;  
X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;  
X<sub>3</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or  
Val;  
X<sub>5</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;  
X<sub>6</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;  
X<sub>7</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;  
X<sub>9</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X<sub>10</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>11</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X<sub>12</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>13</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X<sub>14</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X<sub>16</sub> is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>17</sub> is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X<sub>18</sub> is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Gly-X<sub>9</sub>-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (TN7), wherein

X<sub>1</sub> is Gly or Trp;

X<sub>2</sub> is Ile, Tyr or Val;

X<sub>3</sub> is Gln, Glu, Thr or Trp;

X<sub>5</sub> is Asn, Asp or Glu;

X<sub>6</sub> is Glu, His, Lys or Phe;

X<sub>7</sub> is Asp, Gln, Leu, Lys, Met or Tyr;

X<sub>9</sub> is Arg, Gln, Leu, Lys or Val;

X<sub>11</sub> is Arg, Phe, Ser, Trp or Val;

X<sub>12</sub> is Glu, His or Ser; and

X<sub>13</sub> is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (TN9),

wherein

X<sub>1</sub> is Arg, Asp, Gly, Ile, Met, Pro or Tyr;

X<sub>2</sub> is Asp, Gly, His, Pro or Trp;

X<sub>3</sub> is Gly, Pro, Phe, Thr or Trp;

X<sub>5</sub> is Ala, Asp, Lys, Ser, Trp or Val;

X<sub>6</sub> is Asn, Glu, Gly, His or Leu;

X<sub>7</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X<sub>8</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X<sub>9</sub> is His, Pro or Trp;  
X<sub>10</sub> is Ala, Gly, His, Leu, Trp or Tyr;  
X<sub>11</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp;  
X<sub>13</sub> is Ala, Lys, Ser, Trp or Tyr;  
X<sub>14</sub> is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and  
X<sub>15</sub> is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Ser-Gly-Pro-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub>-Cys-X<sub>17</sub>-X<sub>18</sub>-X<sub>19</sub> (SEQ ID NO:1; MTN13), wherein

X<sub>1</sub> is Arg, Glu, His, Ser or Trp;  
X<sub>2</sub> is Asn, Asp, Leu, Phe, Thr or Val;  
X<sub>3</sub> is Arg, Asp, Glu, His, Lys or Thr;  
X<sub>5</sub> is Asp, Glu, His or Thr;  
X<sub>6</sub> is Arg, His, Lys or Phe;  
X<sub>7</sub> is Gln, Ile, Lys, Tyr or Val;  
X<sub>8</sub> is Gln, Ile, Leu, Met or Phe;  
X<sub>12</sub> is Asn, Asp, Gly, His or Tyr;  
X<sub>13</sub> is Gln, Gly, Ser or Thr;  
X<sub>14</sub> is Glu, Lys, Phe or Ser;  
X<sub>15</sub> is Glu, Ile, Ser or Val;  
X<sub>17</sub> is Glu, Gly, Lys, Phe, Ser or Val;  
X<sub>18</sub> is Arg, Asn, Ser or Tyr; and  
X<sub>19</sub> is Asp, Gln, Glu, Gly, Met or Tyr.

8. (Withdrawn) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 6: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-Tyr-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>, wherein  
X<sub>1</sub> is Ala, Arg, Asp, Leu, Lys, Pro, Ser or Val;  
X<sub>2</sub> is Asn, Asp, Glu, Lys, Thr or Ser;

X<sub>3</sub> is Ile, Leu, Trp;  
X<sub>5</sub> is Ala, Arg, Glu, Lys or Ser;  
X<sub>6</sub> is Ala, Asp, Gln, Glu, Thr or Val;  
X<sub>7</sub> is Asp or Glu;  
X<sub>8</sub> is Trp or Tyr;  
X<sub>9</sub> is Thr or Tyr;  
X<sub>12</sub> is Glu, Met, Phe, Trp or Tyr;  
X<sub>13</sub> is Ile, Leu or Met; and  
X<sub>14</sub> is Ile, Leu, Met, Phe or Thr; or

Consensus Sequence 7: Trp-Tyr-Trp-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Gly-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:2), wherein

X<sub>5</sub> is Asp, Gln or His;  
X<sub>6</sub> is His or Tyr;  
X<sub>7</sub> is Ile, His or Tyr;  
X<sub>9</sub> is Ile, Met or Val;  
X<sub>10</sub> is Gly or Tyr;  
X<sub>12</sub> is Asp, Lys or Pro;  
X<sub>13</sub> is Gln, Gly or Trp; and  
X<sub>14</sub> is Phe, Ser or Thr; or

Consensus Sequence 8: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Gly-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>, wherein

X<sub>1</sub> is Gly, Leu, His, Thr, Trp, Tyr;  
X<sub>2</sub> is Ile, Leu, Thr, Trp or Val;  
X<sub>3</sub> is Asp, Glu, Gln, Trp or Thr;  
X<sub>5</sub> is Ala, Arg, Asn, Asp, His, Phe, Trp or Tyr;  
X<sub>6</sub> is Ala, Asp, Gln, His, Lys, Met, Ser, Thr, Trp, Tyr or Val;

$X_7$  is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr or Val;  
 $X_8$  is Asp, Phe, Ser, Thr, Trp or Tyr;  
 $X_{10}$  is Ala, Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;  
 $X_{12}$  is Arg, Gln, His, Ile, Lys, Met, Phe, Thr, Trp, Tyr or Val;  
 $X_{13}$  is Arg, Asn, Asp, Glu, His, Met, Pro, Ser or Thr; and  
 $X_{14}$  is Arg, Gln, Glu, Gly, Phe, Ser, Trp or Tyr.

9. (Withdrawn) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 9:  $X_1-X_2-X_3-\text{Cys}-X_5-X_6-X_7-X_8-\text{Trp}-\text{Gly}-\text{Gly}-X_{12}-X_{13}-\text{Cys}-X_{15}-X_{16}-X_{17}$   
(SEQ ID NO:3), wherein

$X_1$  is Ser, Phe, Trp, Tyr or Gly;  
 $X_2$  is Arg, Gly, Ser or Trp;  
 $X_3$  is Ala, Glu, Ile or Val;  
 $X_5$  is Ala, Phe or Trp;  
 $X_6$  is Glu or Lys;  
 $X_7$  is Asp, Ser or Trp;  
 $X_8$  is Phe, Pro or Ser;  
 $X_{12}$  is Gln or Glu;  
 $X_{13}$  is Ile, Phe or Val;  
 $X_{15}$  is Gln, Ile, Leu or Phe;  
 $X_{16}$  is Arg, Gly or Pro; and  
 $X_{17}$  is Gln, His, Phe, Ser, Tyr or Val; or

Consensus Sequence 10: Tyr-Pro- $X_3-\text{Cys}-X_5-\text{Glu}-X_7-\text{Ser}-X_9-\text{Ser}-X_{11}-X_{12}-X_{13}-\text{Phe}-\text{Cys}-X_{16}-X_{17}-X_{18}$  (SEQ ID NO:4; TN12), wherein

$X_3$  is Gly or Trp;

X<sub>5</sub> is His or Tyr;

X<sub>7</sub> is His, Leu or Thr;

X<sub>9</sub> is Asp or Leu;

X<sub>11</sub> is Gly or Val;

X<sub>12</sub> is Thr or Val;

X<sub>13</sub> is Arg or Trp;

X<sub>16</sub> is Ala or Val;

X<sub>17</sub> is Asp or Pro; and

X<sub>18</sub> is Gly or Trp; or

Consensus Sequence 11: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Gly-X<sub>12</sub>-Trp-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub> (SEQ ID NO:5; TN12), wherein

X<sub>1</sub> is Asp, Gly, Pro or Ser;

X<sub>2</sub> is Arg, Asn, Asp, Gly or Ser;

X<sub>3</sub> is Gly, Thr, Trp or Tyr;

X<sub>5</sub> is Glu, Met or Thr;

X<sub>6</sub> is Ile, Leu, Met or Phe;

X<sub>7</sub> is Arg, Asp, Glu, Met, Trp or Val;

X<sub>8</sub> is Asn, Gln, Gly, Ser or Val;

X<sub>9</sub> is Asp or Glu;

X<sub>10</sub> is Lys, Ser, Thr or Val;

X<sub>12</sub> is Arg, Gln, Lys or Trp;

X<sub>14</sub> is Asn, Leu, Phe or Tyr;

X<sub>16</sub> is Gly, Phe, Ser or Tyr;

X<sub>17</sub> is Gly, Leu, Pro or Ser; and

X<sub>18</sub> is Ala, Asp, Pro, Ser, Trp or Tyr; or

Consensus Sequence 12: Asn-Trp-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub> (SEQ ID NO:6; TN12), wherein

X<sub>3</sub> is Glu or Lys;

X<sub>5</sub> is Glu or Gly;

X<sub>6</sub> is Trp or Tyr;

X<sub>7</sub> is Ser or Thr;

X<sub>8</sub> is Asn or Gln;

X<sub>9</sub> is Gly or Met;

X<sub>10</sub> is Phe or Tyr;

X<sub>11</sub> is Asp or Gln;

X<sub>12</sub> is Lys or Tyr;

X<sub>13</sub> is Glu or Thr;

X<sub>14</sub> is Glu or Phe;

X<sub>16</sub> is Ala or Val;

X<sub>17</sub> is Arg or Tyr; and

X<sub>18</sub> is Leu or Pro,

wherein the polypeptide binds KDR or a VEGF/KDR complex.

10. (Currently Amended) An isolated polypeptide having the ability to bind to kinase domain region (KDR) or vascular endothelial growth factor/kinase domain region (VEGF/KDR) complex comprising an amino acid sequence of one of the following:

Consensus Sequence 13: Z<sub>1</sub>-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Z<sub>2</sub>; wherein,

Z<sub>1</sub> is a polypeptide of at least one amino acid or is absent;

X<sub>1</sub> is Ala, Asp, Gln or Glu;

X<sub>2</sub> is Ala, Asp, Gln, Glu, Pro;

X<sub>3</sub> is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

X<sub>4</sub> is Asp, Leu, Ser, Trp, Tyr or Val;

X<sub>5</sub> is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

Z<sub>2</sub> is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14: X<sub>1</sub>—X<sub>2</sub>—X<sub>3</sub>—Tyr—Trp—Glu—X<sub>7</sub>—X<sub>8</sub>—X<sub>9</sub>—Leu (SEQ ID NO:7),

wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X<sub>1</sub> is Asp, Gly or Ser;

X<sub>2</sub> is Ile, Phe or Tyr;

X<sub>3</sub> is Ala, Ser or Val;

X<sub>7</sub> is Gln, Glu, Ile or Val;

X<sub>8</sub> is Ala, Ile or Val and;

X<sub>9</sub> is Ala, Glu, Val or Thr; and wherein the polypeptide does not contain Cys residues and wherein the polypeptide is conjugated to one or more detectable labels or therapeutic agents.

11. (Withdrawn) The polypeptide of Claim 7, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 20-86, 87-136, 187-192, 193-203, and 207-259.
12. (Withdrawn) The polypeptide of Claim 10, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NOS: 137-186.
13. (Previously Presented) The polypeptide of claim 10, wherein the polypeptide further comprises N-terminal and/or C-terminal flanking peptides of one or more amino acids.
14. (Previously Presented) The polypeptide of claim 10, wherein the polypeptide comprises a modification selected from the group consisting of: an amino acid substitution, an amide bond substitution, a D-amino acid substitution, a glycosylated amino acid, a disulfide bond, a disulfide mimetic substitution, an amino acid translocation, a retroinverso peptide, a peptoid, a retro-inverso peptoid, and a synthetic peptide.

15. (Previously Presented) The polypeptide of claim 10, wherein the polypeptide further comprises a linker or spacer between the polypeptide and the detectable label or the therapeutic agent.
16. (Original) The polypeptide of Claim 15, wherein the detectable label or the therapeutic agent is selected from the group consisting of: an enzyme, a fluorescent compound, a liposome, an optical dye, one or more paramagnetic metal ions or a superparamagnetic particle, an ultrasound contrast agent and one or more radionuclides.
17. (Original) The polypeptide of Claim 16, wherein the therapeutic agent or detectable label comprises one or more radionuclides.
18. (Original) The polypeptide of Claim 17, wherein the radionuclide is selected from the group consisting of:  $^{18}\text{F}$ ,  $^{124}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{123}\text{I}$ ,  $^{77}\text{Br}$ ,  $^{76}\text{Br}$ ,  $^{99\text{m}}\text{Tc}$ ,  $^{51}\text{Cr}$ ,  $^{67}\text{Ga}$ ,  $^{68}\text{Ga}$ ,  $^{47}\text{Sc}$ ,  $^{51}\text{Cr}$ ,  $^{167}\text{Tm}$ ,  $^{141}\text{Ce}$ ,  $^{111}\text{In}$ ,  $^{168}\text{Yb}$ ,  $^{175}\text{Yb}$ ,  $^{140}\text{La}$ ,  $^{90}\text{Y}$ ,  $^{88}\text{Y}$ ,  $^{153}\text{Sm}$ ,  $^{166}\text{Ho}$ ,  $^{165}\text{Dy}$ ,  $^{166}\text{Dy}$ ,  $^{62}\text{Cu}$ ,  $^{64}\text{Cu}$ ,  $^{67}\text{Cu}$ ,  $^{97}\text{Ru}$ ,  $^{103}\text{Ru}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{203}\text{Pb}$ ,  $^{211}\text{Bi}$ ,  $^{212}\text{Bi}$ ,  $^{213}\text{Bi}$ ,  $^{214}\text{Bi}$ ,  $^{105}\text{Rh}$ ,  $^{109}\text{Pd}$ ,  $^{117\text{m}}\text{Sn}$ ,  $^{149}\text{Pm}$ ,  $^{161}\text{Tb}$ ,  $^{177}\text{Lu}$ ,  $^{198}\text{Au}$  and  $^{199}\text{Au}$ .
19. (Original) The polypeptide of Claim 18, wherein the therapeutic agent or detectable label further comprises a chelator.
20. (Original) The polypeptide of Claim 19, wherein the chelator comprises a compound selected from the group consisting of: formula 20, 21, 22, 23a, 23b, 24a, 24b, and 25.
21. (Original) The polypeptide of Claim 19, wherein the radionuclide is  $^{99\text{m}}\text{Tc}$  or  $^{111}\text{In}$ .
22. (Original) The polypeptide of Claim 19, wherein the radionuclide is selected from the group consisting of:  $^{177}\text{Lu}$ ,  $^{90}\text{Y}$ ,  $^{153}\text{Sm}$  and  $^{166}\text{Ho}$ .

23. (Original) The polypeptide of Claim 16, wherein the detectable label comprises an ultrasound contrast agent.
24. (Original) The polypeptide of Claim 23, wherein the ultrasound contrast agent is a phospholipid stabilized microbubble or an ultrasound contrast agent comprising a gas.
25. (Original) The polypeptide of Claim 24, wherein the ultrasound contrast agent comprises a fluorinated gas.
26. (Original) The polypeptide of Claim 16, wherein the detectable label comprises one or more paramagnetic metal ions and one or more chelators.
27. (Withdrawn) The polypeptide of Claim 15, wherein the therapeutic agent is selected from the group consisting of: a bioactive agent, a cytotoxic agent, a drug, a chemotherapeutic agent and a radiotherapeutic agent.

28-31. (Canceled)

32. (Withdrawn) A method for isolating phage that bind KDR or a VEGF/KDR complex, comprising the steps of:
  - (a) immobilizing a KDR or VEGF/KDR complex target on a solid support;
  - (b) contacting a library of potential KDR or VEGF/KDR complex binding phage with the solid support to bind KDR or a VEGF/KDR complex binding phage in the library; and
  - (c) removing the unbound portion of the phage library from the solid support, thereby isolating phage that bind KDR or a VEGF/KDR complex.

33-52. (Canceled)

53. (Withdrawn) A recombinant bacteriophage displaying a KDR binding or VEGF/KDR complex binding polypeptide, which polypeptide comprises an amino acid sequence of one of the following:

Consensus Sequence 1: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (TN8), wherein

X<sub>1</sub> is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>2</sub> is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>3</sub> is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;  
X<sub>5</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;  
X<sub>6</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>7</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>9</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;  
X<sub>10</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;  
X<sub>12</sub> is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>13</sub> is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and  
X<sub>14</sub> is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub> (TN12), wherein

X<sub>1</sub> is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;  
X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;  
X<sub>3</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>5</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;  
X<sub>6</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X<sub>7</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;  
X<sub>9</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>10</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>11</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;  
X<sub>12</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>13</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;  
X<sub>14</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;  
X<sub>16</sub> is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>17</sub> is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and  
X<sub>18</sub> is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Gly-X<sub>9</sub>-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (TN7), wherein

X<sub>1</sub> is Gly or Trp;  
X<sub>2</sub> is Ile, Tyr or Val;  
X<sub>3</sub> is Gln, Glu, Thr or Trp;  
X<sub>5</sub> is Asn, Asp or Glu;  
X<sub>6</sub> is Glu, His, Lys or Phe;  
X<sub>7</sub> is Asp, Gln, Leu, Lys, Met or Tyr;  
X<sub>9</sub> is Arg, Gln, Leu, Lys or Val;  
X<sub>11</sub> is Arg, Phe, Ser, Trp or Val;  
X<sub>12</sub> is Glu, His or Ser; and  
X<sub>13</sub> is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (TN9), wherein

X<sub>1</sub> is Arg, Asp, Gly, Ile, Met, Pro or Tyr;  
X<sub>2</sub> is Asp, Gly, His, Pro or Trp;  
X<sub>3</sub> is Gly, Pro, Phe, Thr or Trp;  
X<sub>5</sub> is Ala, Asp, Lys, Ser, Trp or Val;

X<sub>6</sub> is Asn, Glu, Gly, His or Leu;  
X<sub>7</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;  
X<sub>8</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;  
X<sub>9</sub> is His, Pro or Trp;  
X<sub>10</sub> is Ala, Gly, His, Leu, Trp or Tyr;  
X<sub>11</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp;  
X<sub>13</sub> is Ala, Lys, Ser, Trp or Tyr;  
X<sub>14</sub> is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and  
X<sub>15</sub> is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Ser-Gly-Pro-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub>-Cys-X<sub>17</sub>-X<sub>18</sub>-X<sub>19</sub> (SEQ ID NO:1; MTN13), wherein

X<sub>1</sub> is Arg, Glu, His, Ser or Trp;  
X<sub>2</sub> is Asn, Asp, Leu, Phe, Thr or Val;  
X<sub>3</sub> is Arg, Asp, Glu, His, Lys or Thr;  
X<sub>5</sub> is Asp, Glu, His or Thr;  
X<sub>6</sub> is Arg, His, Lys or Phe;  
X<sub>7</sub> is Gln, Ile, Lys, Tyr or Val;  
X<sub>8</sub> is Gln, Ile, Leu, Met or Phe;  
X<sub>12</sub> is Asn, Asp, Gly, His or Tyr;  
X<sub>13</sub> is Gln, Gly, Ser or Thr;  
X<sub>14</sub> is Glu, Lys, Phe or Ser;  
X<sub>15</sub> is Glu, Ile, Ser or Val;  
X<sub>17</sub> is Glu, Gly, Lys, Phe, Ser or Val;  
X<sub>18</sub> is Arg, Asn, Ser or Tyr; and  
X<sub>19</sub> is Asp, Gln, Glu, Gly, Met or Tyr,

and wherein the polypeptide is displayed on the surface of the recombinant bacteriophage.

54. (Withdrawn) A magnetic resonance imaging contrast agent comprising a KDR or VEGF/KDR complex binding polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (TN8),

wherein

X<sub>1</sub> is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>2</sub> is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>3</sub> is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X<sub>5</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X<sub>6</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>7</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>8</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X<sub>9</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X<sub>10</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X<sub>12</sub> is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>13</sub> is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X<sub>14</sub> is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub> (TN12), wherein

X<sub>1</sub> is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X<sub>3</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>5</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X<sub>6</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X<sub>7</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

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X<sub>8</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;  
X<sub>9</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>10</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>11</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;  
X<sub>12</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>13</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;  
X<sub>14</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;  
X<sub>16</sub> is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>17</sub> is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and  
X<sub>18</sub> is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Gly-X<sub>9</sub>-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (TN7), wherein

X<sub>1</sub> is Gly or Trp;  
X<sub>2</sub> is Ile, Tyr or Val;  
X<sub>3</sub> is Gln, Glu, Thr or Trp;  
X<sub>5</sub> is Asn, Asp or Glu;  
X<sub>6</sub> is Glu, His, Lys or Phe;  
X<sub>7</sub> is Asp, Gln, Leu, Lys, Met or Tyr;  
X<sub>9</sub> is Arg, Gln, Leu, Lys or Val;  
X<sub>11</sub> is Arg, Phe, Ser, Trp or Val;  
X<sub>12</sub> is Glu, His or Ser; and  
X<sub>13</sub> is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (TN9), wherein

X<sub>1</sub> is Arg, Asp, Gly, Ile, Met, Pro or Tyr;  
X<sub>2</sub> is Asp, Gly, His, Pro or Trp;  
X<sub>3</sub> is Gly, Pro, Phe, Thr or Trp;  
X<sub>5</sub> is Ala, Asp, Lys, Ser, Trp or Val;  
X<sub>6</sub> is Asn, Glu, Gly, His or Leu;

X<sub>7</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;  
X<sub>8</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;  
X<sub>9</sub> is His, Pro or Trp;  
X<sub>10</sub> is Ala, Gly, His, Leu, Trp or Tyr;  
X<sub>11</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp;  
X<sub>13</sub> is Ala, Lys, Ser, Trp or Tyr;  
X<sub>14</sub> is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and  
X<sub>15</sub> is Asn, Gln, Glu, Leu, Met, Pro or Trp; or

Consensus Sequence 5: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Ser-Gly-Pro-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub>-Cys-X<sub>17</sub>-X<sub>18</sub>-X<sub>19</sub> (SEQ ID NO:1; MTN13), wherein

X<sub>1</sub> is Arg, Glu, His, Ser or Trp;  
X<sub>2</sub> is Asn, Asp, Leu, Phe, Thr or Val;  
X<sub>3</sub> is Arg, Asp, Glu, His, Lys or Thr;  
X<sub>5</sub> is Asp, Glu, His or Thr;  
X<sub>6</sub> is Arg, His, Lys or Phe;  
X<sub>7</sub> is Gln, Ile, Lys, Tyr or Val;  
X<sub>8</sub> is Gln, Ile, Leu, Met or Phe;  
X<sub>12</sub> is Asn, Asp, Gly, His or Tyr;  
X<sub>13</sub> is Gln, Gly, Ser or Thr;  
X<sub>14</sub> is Glu, Lys, Phe or Ser;  
X<sub>15</sub> is Glu, Ile, Ser or Val;  
X<sub>17</sub> is Glu, Gly, Lys, Phe, Ser or Val;  
X<sub>18</sub> is Arg, Asn, Ser or Tyr; and  
X<sub>19</sub> is Asp, Gln, Glu, Gly, Met or Tyr,

wherein the polypeptide is coupled to at least one chelator capable of complexing a paramagnetic metal or at least one superparamagnetic particle, and wherein the polypeptide optionally comprises an N-terminal and/or C-terminal flanking peptide.

55-75. (Canceled)

76. (Withdrawn) A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid selected from the group consisting of:

Loop Consensus Sequence 15: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Cys (TN8), wherein  
X<sub>2</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;  
X<sub>3</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>4</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>5</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>6</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and  
X<sub>7</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys (TN12), wherein

X<sub>2</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;  
X<sub>3</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;  
X<sub>4</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>5</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;  
X<sub>6</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>7</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;  
X<sub>9</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>10</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and  
X<sub>11</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Gly-X<sub>6</sub>-Cys (TN7), wherein

X<sub>2</sub> is Asn, Asp or Glu;  
X<sub>3</sub> is Glu, His, Lys or Phe;  
X<sub>4</sub> is Asp, Gln, Leu, Lys, Met or Tyr; and

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X<sub>6</sub> is Arg, Gln, Leu, Lys or Val; or

Consensus Sequence IV: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (TN9), wherein

X<sub>2</sub> is Ala, Asp, Lys, Ser, Trp or Val;

X<sub>3</sub> is Asn, Glu, Gly, His or Leu;

X<sub>4</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X<sub>5</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X<sub>6</sub> is His, Pro or Trp;

X<sub>7</sub> is Ala, Gly, His, Leu, Trp or Tyr; and

X<sub>8</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 18: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (TN9), wherein

X<sub>2</sub> is Ala, Asp, Lys, Ser, Trp or Val;

X<sub>3</sub> is Asn, Glu, Gly, His or Leu;

X<sub>4</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X<sub>5</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X<sub>6</sub> is His, Pro or Trp;

X<sub>7</sub> is Ala, Gly, His, Leu, Trp or Tyr; and

X<sub>8</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Ser-Gly-Pro-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys

(MTN13; SEQ ID NO:1), wherein

X<sub>2</sub> is Asp, Glu, His or Thr;

X<sub>3</sub> is Arg, His, Lys or Phe;

X<sub>4</sub> is Gln, Ile, Lys, Tyr or Val;

X<sub>5</sub> is Gln, Ile, Leu, Met or Phe;

X<sub>9</sub> is Asn, Asp, Gly, His or Tyr;

X<sub>10</sub> is Gln, Gly, Ser or Thr;

X<sub>11</sub> is Glu, Lys, Phe or Ser; and

X<sub>12</sub> is Glu, Ile, Ser or Val.

77. (Canceled)

78. (Currently Amended) A multimeric polypeptide construct having the ability to bind to KDR or VEGF/KDR complex comprising at least one amino acid sequence of one of the following:

Consensus Sequence 13:  $Z_1-X_1-X_2-X_3-X_4-X_5-Z_2$ ; wherein,

$Z_1$  is a polypeptide of at least one amino acid or is absent;

$X_1$  is Ala, Asp, Gln or Glu;

$X_2$  is Ala, Asp, Gln, Glu, Pro;

$X_3$  is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;

$X_4$  is Asp, Leu, Ser, Trp, Tyr or Val;

$X_5$  is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and

$Z_2$  is a polypeptide of at least one amino acid or is absent; or

Consensus Sequence 14:  $X_1-X_2-X_3-Tyr-Trp-Glu-X_7-X_8-X_9-Leu$  (SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

$X_1$  is Asp, Gly or Ser;

$X_2$  is Ile, Phe or Tyr;

$X_3$  is Ala, Ser or Val;

$X_7$  is Gln, Glu, Ile or Val;

$X_8$  is Ala, Ile or Val and;

$X_9$  is Ala, Glu, Val or Thr, wherein the polypeptide does not contain Cys residues.

79-157. (Canceled)

158. (Withdrawn) A method of detecting KDR or VEGF/KDR complex in an animal or human subject and optionally imaging at least a portion of the animal or human subject comprising the steps of:

- (a) detectably labeling a multimeric polypeptide construct of one of Claims 76, or 78;
- (b) administering to the subject the labeled multimeric polypeptide construct; and,
- (c) detecting the labeled multimeric polypeptide construct in the subject, and, optionally, constructing an image..

159-174. (Canceled)

175. (Withdrawn) A multimeric polypeptide having the ability to bind to KDR or VEGF/KDR complex selected from the group consisting of: D30 and D31.

176-194. (Canceled)

195. (Withdrawn) A method of inhibiting VEGF activation of KDR comprising administering to an animal or human subject in need of treatment for such condition a polypeptide having the ability to bind to KDR or VEGF/KDR complex, or a multimeric polypeptide construct comprising at least one polypeptide having the ability to bind to KDR or VEGF/KDR complex, said polypeptide comprising an amino acid sequence of one of the following:

Consensus Sequence 1: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (TN8),

wherein

X<sub>1</sub> is Ala, Arg, Asp, Gly, His, Leu, Lys, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>2</sub> is Asn, Asp, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>3</sub> is Asn, Asp, Gln, Glu, Ile, Leu, Met, Thr, Trp or Val;

X<sub>5</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;

X<sub>6</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>7</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>8</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;

X<sub>9</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val;

X<sub>10</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr;

X<sub>12</sub> is Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>13</sub> is Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp or Tyr; and

X<sub>14</sub> is Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr; or

Consensus Sequence 2: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub> (TN12), wherein

X<sub>1</sub> is Ala, Asn, Asp, Gly, Leu, Pro, Ser, Trp or Tyr;

X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr;

X<sub>3</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>5</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;

X<sub>6</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;

X<sub>7</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>8</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;

X<sub>9</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;

X<sub>10</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;

X<sub>11</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;

X<sub>12</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>13</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val;

X<sub>14</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val;

X<sub>16</sub> is Ala, Asn, Asp, Gln, Glu, Gly, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;

X<sub>17</sub> is Arg, Asn, Asp, Cys, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X<sub>18</sub> is Ala, Asn, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp or Tyr; or

Consensus Sequence 3: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Gly-X<sub>9</sub>-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (TN7), wherein

X<sub>1</sub> is Gly or Trp;

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X<sub>2</sub> is Ile, Tyr or Val;  
X<sub>3</sub> is Gln, Glu, Thr or Trp;  
X<sub>5</sub> is Asn, Asp or Glu;  
X<sub>6</sub> is Glu, His, Lys or Phe;  
X<sub>7</sub> is Asp, Gln, Leu, Lys, Met or Tyr;  
X<sub>9</sub> is Arg, Gln, Leu, Lys or Val;  
X<sub>11</sub> is Arg, Phe, Ser, Trp or Val;  
X<sub>12</sub> is Glu, His or Ser; and  
X<sub>13</sub> is Glu, Gly, Trp or Tyr; or

Consensus Sequence 4: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (TN9),  
wherein

X<sub>1</sub> is Arg, Asp, Gly, Ile, Met, Pro or Tyr;  
X<sub>2</sub> is Asp, Gly, His, Pro or Trp;  
X<sub>3</sub> is Gly, Pro, Phe, Thr or Trp;  
X<sub>5</sub> is Ala, Asp, Lys, Ser, Trp or Val;  
X<sub>6</sub> is Asn, Glu, Gly, His or Leu;  
X<sub>7</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;  
X<sub>8</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;  
X<sub>9</sub> is His, Pro or Trp;  
X<sub>10</sub> is Ala, Gly, His, Leu, Trp or Tyr;  
X<sub>11</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp;  
X<sub>13</sub> is Ala, Lys, Ser, Trp or Tyr;  
X<sub>14</sub> is Asp, Gly, Leu, His, Met, Thr, Trp or Tyr; and  
X<sub>15</sub> is Asn, Gln, Glu, Leu, Met, Pro or Trp;

Consensus Sequence 5: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Ser-Gly-Pro-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub>-Cys-X<sub>17</sub>-X<sub>18</sub>-X<sub>19</sub> (SEQ ID NO:1; MTN13), wherein

X<sub>1</sub> is Arg, Glu, His, Ser or Trp;  
X<sub>2</sub> is Asn, Asp, Leu, Phe, Thr or Val;  
X<sub>3</sub> is Arg, Asp, Glu, His, Lys or Thr;

X<sub>5</sub> is Asp, Glu, His or Thr;  
X<sub>6</sub> is Arg, His, Lys or Phe;  
X<sub>7</sub> is Gln, Ile, Lys, Tyr or Val;  
X<sub>8</sub> is Gln, Ile, Leu, Met or Phe;  
X<sub>12</sub> is Asn, Asp, Gly, His or Tyr;  
X<sub>13</sub> is Gln, Gly, Ser or Thr;  
X<sub>14</sub> is Glu, Lys, Phe or Ser;  
X<sub>15</sub> is Glu, Ile, Ser or Val;  
X<sub>17</sub> is Glu, Gly, Lys, Phe, Ser or Val;  
X<sub>18</sub> is Arg, Asn, Ser or Tyr; and  
X<sub>19</sub> is Asp, Gln, Glu, Gly, Met or Tyr;

Consensus Sequence 13: Z<sub>1</sub>-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Z<sub>2</sub> (Lin20); wherein,

Z<sub>1</sub> is a polypeptide of at least one amino acid or is absent;  
X<sub>1</sub> is Ala, Asp, Gln or Glu;  
X<sub>2</sub> is Ala, Asp, Gln, Glu, Pro;  
X<sub>3</sub> is Ala, Leu, Lys, Phe, Pro, Trp or Tyr;  
X<sub>4</sub> is Asp, Leu, Ser, Trp, Tyr or Val;  
X<sub>5</sub> is Ala, Arg, Asp, Glu, Gly, Leu, Trp or Tyr; and  
Z<sub>2</sub> is a polypeptide of at least one amino acid or is absent;

Consensus Sequence 14: X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Tyr-Trp-Glu-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-Leu (Lin20; SEQ ID NO:7), wherein, the sequence can optionally have a N-terminal polypeptide, C-terminal polypeptide, or a polypeptide at both termini of at least one amino acid; wherein,

X<sub>1</sub> is Asp, Gly or Ser;  
X<sub>2</sub> is Ile, Phe or Tyr;  
X<sub>3</sub> is Ala, Ser or Val;  
X<sub>7</sub> is Gln, Glu, Ile or Val;  
X<sub>8</sub> is Ala, Ile or Val;  
X<sub>9</sub> is Ala, Glu, Val or Thr;

Loop Consensus Sequence 15: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Cys (TN8), wherein

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X<sub>2</sub> is Ala, Arg, Asn, Asp, Gln, Glu, His, Ile, Lys, Phe, Pro, Ser, Trp or Tyr;  
X<sub>3</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>4</sub> is Ala, Asn, Asp, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val (preferably Asp);  
X<sub>5</sub> is Ala, Asp, Glu, Gly, Leu, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>6</sub> is Arg, Gln, Glu, Gly, Ile, Leu, Met, Pro, Thr, Trp, Tyr or Val; and  
X<sub>7</sub> is Ala, Arg, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Trp or Tyr; or

Loop Consensus Sequence 16:Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys (TN12), wherein  
X<sub>2</sub> is Arg, Asp, Gln, Glu, Gly, His, Ile, Lys, Met, Thr, Trp, Tyr or Val;  
X<sub>3</sub> is Ala, Arg, Asn, Cys, Glu, Ile, Leu, Met, Phe, Ser, Trp or Tyr;  
X<sub>4</sub> is Arg, Asn, Asp, Gln, Glu, His, Ile, Leu, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>5</sub> is Ala, Asn, Asp, Gln, Glu, Gly, His, Met, Phe, Pro, Ser, Trp, Tyr or Val;  
X<sub>6</sub> is Asp, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp or Tyr;  
X<sub>7</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val;  
X<sub>8</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Lys, Trp, Tyr or Val;  
X<sub>9</sub> is Ala, Arg, Gln, Gly, His, Ile, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val;  
X<sub>10</sub> is Arg, Gln, Glu, His, Leu, Lys, Met, Phe, Pro, Thr, Trp or Val; and  
X<sub>11</sub> is Arg, Asn, Asp, Glu, His, Ile, Leu, Met, Phe, Pro, Thr, Trp, Tyr or Val; or

Loop Consensus Sequence 17: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Gly-X<sub>6</sub>-Cys (TN7), wherein

X<sub>2</sub> is Asn, Asp or Glu;  
X<sub>3</sub> is Glu, His, Lys or Phe;  
X<sub>4</sub> is Asp, Gln, Leu, Lys, Met or Tyr; and  
X<sub>6</sub> is Arg, Gln, Leu, Lys or Val; or

Loop Consensus Sequence 18: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (TN9), wherein

X<sub>2</sub> is Ala, Asp, Lys, Ser, Trp or Val;  
X<sub>3</sub> is Asn, Glu, Gly, His or Leu;  
X<sub>4</sub> is Gln, Glu, Gly, Met, Lys, Phe, Tyr or Val;

X<sub>5</sub> is Ala, Asn, Asp, Gly, Leu, Met, Pro, Ser or Thr;

X<sub>6</sub> is His, Pro or Trp;

X<sub>7</sub> is Ala, Gly, His, Leu, Trp or Tyr; and

X<sub>8</sub> is Ala, Asp, Gln, Leu, Met, Thr or Trp; or

Loop Consensus Sequence 19: Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-Ser-Gly-Pro-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys  
(MTN13; SEQ ID NO:1), wherein

X<sub>2</sub> is Asp, Glu, His or Thr;

X<sub>3</sub> is Arg, His, Lys or Phe;

X<sub>4</sub> is Gln, Ile, Lys, Tyr or Val;

X<sub>5</sub> is Gln, Ile, Leu, Met or Phe;

X<sub>9</sub> is Asn, Asp, Gly, His or Tyr;

X<sub>10</sub> is Gln, Gly, Ser or Thr;

X<sub>11</sub> is Glu, Lys, Phe or Ser; and

X<sub>12</sub> is Glu, Ile, Ser or Val.

196-197. (Canceled)

198. (Currently Amended) An isolated polypeptide having the ability to bind to kinase domain region (KDR) or vascular endothelial growth factor/kinase domain region (VEGF/KDR) complex comprising an amino acid sequence of ~~SEQ ID NO.:304, SEQ ID NO.:305, SEQ ID NO.:306, SEQ ID NO.:307, SEQ ID NO.:308, SEQ ID NO.:309, or SEQ ID NO.:310~~ SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, or SEQ ID NO:310.

199. (Currently Amended) The isolated polypeptide of claim 198, wherein the polypeptide consists of the amino acid sequence ~~SEQ ID NO.:310~~ SEQ ID NO:310.